Claims Listing:

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1.-20. (Cancelled)

21. (Currently amended) A method to detect expression of a HAS1 isoenzyme variants, wherein the HAS1 isoenzyme variant is SEQ ID NO. 4 comprising:

i) mixing a cell or sample of cell populate from a human with reverse transcriptase in conditions enabling conversion of mRNA to DNA templates thereby generating cDNA templates;

ii) mixing said cDNA templates with oligonucleotide primers SEQ ID NO:9 and SEQ ID NO: 10;

a. Reacting said mixture ii with enzymes and compounds to enable specific fragments of DNA to be increased in number;

b. Detecting the presence of an increased number of resulting DNA fragments of ~~particular size associated with the presence of~~ 86 base pairs from SEQ ID NO:3.

22 - 26 (Cancelled)

27. (Previously presented) The method of claim 21 wherein the process is performed using a microfluidic device.

28. (Previously presented) A method to detect expression of HAS1Va isoenzyme variant in a cell or cell population comprising detection of single nucleotide conversion of base 924 of SEQ ID NO:3 from a cytosine to a thymidine residue.

29 - 48. (Cancelled)

49. (Currently amended) A method to determine the likelihood of ~~poor clinical outcome~~ survival rate over time in a human suffering from multiple myeloma comprising characterizing HAS1Va isoenzyme variant expression in a cell or cell population using the method of claim 21, wherein the HAS1Va isoenzyme variant is SEQ ID NO. 4.

50. (Previously presented) The method of claim 49 wherein the cell or cell population is selected from the group comprising blood, B-cells, CD 19.sup.+ B cells, CD 19.sup.+ peripheral blood mononuclear cells and bone marrow plasma cells.

51 - 106 (Cancelled)